SEQUENCE LISTING

<110> Medical & Biological Laboratories Co.,Ltd.

<120> Thioredoxin reductase II

<130> M3-007PCT

<140>
<141>

<150> JP   1998-310422
<151> 1998-10-30

<160> 37

<170> PatentIn Ver. 2.0

<210> 1
<211> 1959
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (10)..(1572)

<220>
<221> misc_structure
<222> (1567)..(1569)

<220>
<221> misc_structure
<222> (1664)..(1666)
<223> tga is transrated to selenosysteine, shown by Xaa.

<400> 1
atggcggca atg gcg gtg gcg ctg cgg gga tta gga ggg cgc ttc cgg tgg   51
          Met Ala Val Ala Leu Arg Gly Leu Gly Gly Arg Phe Arg Trp
            1   5   10

cgg acg cag gcc gtg gcg ggc ggg gtg cgg ggc gcg gcg cgg ggc gca   99
Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala
 15   20   25   30

gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct   147
Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser
                35   40   45

ggt ggc ctg gct tgt gcc aag gag gcc gcc cag ctg gga agg aag gtg   195
Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val
            50   55   60

gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc   243

```
Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly
         65                  70               75


ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg    291
Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met
         80                  85               90


cac cag gcg gca ctg ctg gga ggc ctg atc caa gat gcc ccc aac tat    339
His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr
 95                  100              105              110


ggc tgg gag gtg gcc cag ccc gtg ccg cat gac tgg agg aag atg gca    387
Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala
                115              120              125


gaa gct gtt caa aat cac gtg aaa tcc ttg aac tgg ggc cac cgt gtc    435
Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val
                130              135              140


cag ctt cag gac aga aaa gtc aag tac ttt aac atc aaa gcc agc ttt    483
Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe
            145              150              155


gtt gac gag cac acg gtt tgc ggc gtt gcc aaa ggt ggg aaa gag att    531
Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile
            160              165              170


ctg ctg tca gcc gat cac atc atc att gct act gga ggg cgg ccg aga    579
Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg
175              180              185              190


tac ccc acg cac atc gaa ggt gcc ttg gaa tat gga atc aca agt gat    627
Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp
                195              200              205


gac atc ttc tgg ctg aag gaa tcc cct gga aaa acg ttg gtg gtc ggg    675
Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly
            210              215              220


gcc agc tat gtg gcc ctg gag tgt gct ggc ttc ctc acc ggg att ggg    723
Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly
            225              230              235


ctg gac acc acc atc atg atg cgc agc atc ccc ctc cgc ggc ttc gac    771
Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp
            240              245              250


cag caa atg tcc tcc atg gtc ata gag cac atg gca tct cat ggc acc    819
Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr
255              260              265              270


cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc agg agg ctc cct gat    867
Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp
                275              280              285


ggc cag ctg cag gtc acc tgg gag gac agc acc acc ggc aag gag gac    915
Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp
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acg ggc acc ttt gac acc gtc ctg tgg gcc ata ggt cga gtc cca gac   963
Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp
        305                    310                    315

acc aga agt ctg aat ttg gag aag gct ggg gta gat act agc ccc gac  1011
Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp
        320                    325                    330

act cag aag atc ctg gtg gac tcc cgg gaa gcc acc tct gtg ccc cac  1059
Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His
335                    340                    345                    350

atc tac gcc att ggt gac gtg gtg gag ggg cgg cct gag ctg aca ccc  1107
Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro
                355                    360                    365

aca gcg atc atg gcc ggg agg ctc ctg gtg cag cgg ctc ttc ggc ggg  1155
Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly
            370                    375                    380

tcc tca gat ctg atg gac tac gac aat gtt ccc acg acc gtc ttc acc  1203
Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr
        385                    390                    395

cca ctg gag tat ggc tgt gtg ggg ctg tcc gag gag gag gca gtg gct  1251
Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala
        400                    405                    410

cgc cac ggg cag gag cat gtt gag gtc tat cac gcc cat tat aaa cca  1299
Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro
415                    420                    425                    430

ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag  1347
Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys
                435                    440                    445

atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc  1395
Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe
            450                    455                    460

ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc  1443
Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile
        465                    470                    475

aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat  1491
Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His
        480                    485                    490

ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca  1539
Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser
495                    500                    505                    510

ggc ctg gac ccc acg gtg aca ggc tgc tga ggg taagcgccat ccctgcaggc 1592
Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
                515                    520
```

caggggcacac ggtgcgcccg ccgccagctc ctcggaggcc agacccagga tggctgcagg 1652

ccaggtttgg ggggcctcaa ccctctcctg gagcgcctgt gagatggtca gcgtggagcg 1712

caagtgctgg acgggtggcc cgtgtgcccc acagggatgg ctcaggggac tgtccacctc 1772

acccctgcac ctttcagcct ttgccgccgg caccccccc caggctcctg gtgccggatg 1832

atgacgacct gggtggaaac ctaccctgtg ggcacccatg tccgagcccc ctggcatttc 1892

tgcaatgcaa ataaagaggg tactttttct gaagtgtgta aaaaaaaaa aaaaaaaaa 1952

aaaaaaa   1959

<210> 2
<211> 521
<212> PRT
<213> Homo sapiens
<223> Xaa(520) means selenosysteine.

<400> 2
Met Ala Val Ala Leu Arg Gly Leu Gly Gly Arg Phe Arg Trp Arg Thr
 1   5   10   15

Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala Ala Ala
                20   25   30

Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser Gly Gly
            35   40   45

Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val
        50   55   60

Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly
 65   70   75   80

Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln
                85   90   95

Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp
            100   105   110

Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala
        115   120   125

Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu
    130   135   140

Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp
145   150   155   160

Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu
                165   170   175

Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg Tyr Pro

```
                180                      185                      190

     Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp Asp Ile
             195                     200                     205

     Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly Ala Ser
             210                     215                     220

     Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly Leu Asp
     225                     230                     235                     240

     Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp Gln Gln
                     245                     250                     255

     Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr Arg Phe
                     260                     265                     270

     Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp Gly Gln
             275                     280                     285

     Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp Thr Gly
             290                     295                     300

     Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp Thr Arg
     305                     310                     315                     320

     Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp Thr Gln
                     325                     330                     335

     Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His Ile Tyr
                     340                     345                     350

     Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro Thr Ala
                     355                     360                     365

     Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly Ser Ser
             370                     375                     380

     Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr Pro Leu
     385                     390                     395                     400

     Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His
                     405                     410                     415

     Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu
                     420                     425                     430

     Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
             435                     440                     445

     Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
             450                     455                     460

     Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
     465                     470                     475                     480

     Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
```

```
Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser Gly Leu
          500                  505                  510

Asp Pro Thr Val Thr Gly Cys Xaa Gly
          515                  520


<210> 3
<211> 2056
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (188)..(1669)
<223> tga(1664)..(1666) is transrated to selenosysteine, shown by Xaa.

<400> 3
gtcccggacc tcaggcccag ttcagtgtac ttcccctctc tacttcctcc ctccagtccc 60

ttctccatcc ctcccttttt tggctgcccc ttgcctgcct tcctcgccag tagcttgcag 120

agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180

agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg   229
        Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
         1               5                  10

gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag   277
Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
 15               20                  25                  30

ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa   325
Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
             35                  40                  45

ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc   373
Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
             50                  55                  60

ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa   421
Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
         65                  70                  75

gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac   469
Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
     80                  85                  90

tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac   517
Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn
 95                  100                 105                 110

tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac   565
Trp Gly His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn
             115                 120                 125
```

```
atc aaa gcc agc ttt gtt gac gag cac acg gtt tgc ggc gtt gcc aaa    613
Ile Lys Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys
            130                 135                 140

ggt ggg aaa gag att ctg ctg tca gcc gat cac atc atc att gct act    661
Gly Gly Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr
            145                 150                 155

gga ggg cgg ccg aga tac ccc acg cac atc gaa ggt gcc ttg gaa tat    709
Gly Gly Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr
            160                 165                 170

gga atc aca agt gat gac atc ttc tgg ctg aag gaa tcc cct gga aaa    757
Gly Ile Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys
175                 180                 185                 190

acg ttg gtg gtc ggg gcc agc tat gtg gcc ctg gag tgt gct ggc ttc    805
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
                    195                 200                 205

ctc acc ggg att ggg ctg gac acc acc atc atg atg cgc agc atc ccc    853
Leu Thr Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro
                210                 215                 220

ctc cgc ggc ttc gac cag caa atg tcc tcc atg gtc ata gag cac atg    901
Leu Arg Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met
            225                 230                 235

gca tct cat ggc acc cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc    949
Ala Ser His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val
            240                 245                 250

agg agg ctc cct gat ggc cag ctg cag gtc acc tgg gag gac agc acc    997
Arg Arg Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr
255                 260                 265                 270

acc ggc aag gag gac acg ggc acc ttt gac acc gtc ctg tgg gcc ata   1045
Thr Gly Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile
            275                 280                 285

ggt cga gtc cca gac acc aga agt ctg aat ttg gag aag gct ggg gta   1093
Gly Arg Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val
            290                 295                 300

gat act agc ccc gac act cag aag atc ctg gtg gac tcc cgg gaa gcc   1141
Asp Thr Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala
            305                 310                 315

acc tct gtg ccc cac atc tac gcc att ggt gac gtg gtg gag ggg cgg   1189
Thr Ser Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg
            320                 325                 330

cct gag ctg aca ccc aca gcg atc atg gcc ggg agg ctc ctg gtg cag   1237
Pro Glu Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln
335                 340                 345                 350
```

```
cgg ctc ttc ggc ggg tcc tca gat ctg atg gac tac gac aat gtt ccc    1285
Arg Leu Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro
                355                 360                 365

acg acc gtc ttc acc cca ctg gag tat ggc tgt gtg ggg ctg tcc gag    1333
Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu
                370                 375                 380

gag gag gca gtg gct cgc cac ggg cag gag cat gtt gag gtc tat cac    1381
Glu Glu Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His
                385                 390                 395

gcc cat tat aaa cca ctg gag ttc acg gtg gct gga cga gat gca tcc    1429
Ala His Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser
        400                 405                 410

cag tgt tat gta aag atg gtg tgc ctg agg gag ccc cca cag ctg gtg    1477
Gln Cys Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val
415                 420                 425                 430

ctg ggc ctg cat ttc ctt ggc ccc aac gca ggc gaa gtt act caa gga    1525
Leu Gly Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly
                435                 440                 445

ttt gct ctg ggg atc aag tgt ggg gct tcc tat gcg cag gtg atg cgg    1573
Phe Ala Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg
                450                 455                 460

acc gtg ggt atc cat ccc aca tgc tct gag gag gta gtc aag ctg cgc    1621
Thr Val Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg
                465                 470                 475

atc tcc aag cgc tca ggc ctg gac ccc acg gtg aca ggc tgc tga ggg    1669
Ile Ser Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
        480                 485                 490

taagcgccat ccctgcaggc cagggcacac ggtgcgcccg ccgccagctc ctcggaggcc 1729

agacccagga tggctgcagg ccaggtttgg ggggcctcaa ccctctcctg gagcgcctgt 1789

gagatggtca gcgtggagcg caagtgctgg acgggtggcc cgtgtgcccc acagggatgg 1849

ctcaggggac tgtccacctc acccctgcac ctttcagcct ttgccgccgg gcaccccccc 1909

caggctcctg gtgccggatg atgacgacct gggtggaaac ctaccctgtg ggcacccatg 1969

tccgagcccc ctggcatttc tgcaatgcaa ataaagaggg tactttttct gaagtgtgta 2029

aaaaaaaaaa aaaaaaaaaa aaaaaaa                                      2056


<210> 4
<211> 492
<212> PRT
<213> Homo sapiens
<223> Xaa(493) means selenosysteine.
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<400> 4

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Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly
 1               5                  10                  15

Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly
            20                  25                  30

Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr
        35                  40                  45

Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys
    50                  55                  60

Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala
65                  70                  75                      80

Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg
            85                  90                  95

Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly
            100                 105                 110

His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys
        115                 120                 125

Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly
    130                 135                 140

Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly
145                 150                 155                     160

Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile
            165                 170                 175

Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu
            180                 185                 190

Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr
    195                 200                 205

Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg
    210                 215                 220

Gly Phe Asp Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser
225                 230                 235                     240

His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg
            245                 250                 255

Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly
            260                 265                 270

Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg
            275                 280                 285

Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr
    290                 295                 300
```

```
Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser
305             310             315             320

Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu
            325             330             335

Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu
            340             345             350

Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr
            355             360             365

Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu
        370             375             380

Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His
385             390             395             400

Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys
            405             410             415

Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly
            420             425             430

Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala
        435             440             445

Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val
    450             455             460

Gly Ile His Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser
465             470             475             480

Lys Arg Ser Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
            485             490

<210> 5
<211> 130
<212> DNA
<213> Homo sapiens

<400> 5
tcagcctttg ccgccgggca cccccccag gctcctggtg ccggatgatg acgacctggg 60

tggaaaccta ccctgtgggc acccatgtcc gagcccctg gcattctgc aatgcaaata 120

aagagggtac                                                       130


<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence:Synthesis

<400> 6
gcgggatcca tgactttttaa cagttttgaa gg   32

<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 7
gcgctcgagc tactatagag ttagattaag ac   32

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 8
tatgatctcc tggtggtc   18

<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 9
gtcatcactt gtgattcc   18

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 10
acagcttctg ccatcttcct c   21

<210> 11
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 11
agaaggttcc acgtagtcca c   21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthesis

<400> 12
ccatacgatg ttccagatta c   21

<210> 13
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence:synthesis

<400> 13
acgatggcgg caatggcggt g   21

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 14
accatggagg accaagcagg t   21

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 15
ttaccctcag cagcctgtca c   21

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<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 16
gcgccatccc tgcaggccag g                                              21


<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthesis

<400> 17
cacacttcag aaaaagtacc c                                              21


<210> 18
<211> 103
<212> DNA
<213> Homo sapiens

<400> 18
atggcggcaa tggcggtggc gctgcgggga ttaggagggc gcttccggtg gcggacgcag 60

gccgtggcgg gcggggtgcg gggcgcggcg cggggcgcag cag                     103


<210> 19
<211> 200
<212> DNA
<213> Homo sapiens

<400> 19
gtcccggacc tcaggcccag ttcagtgtac ttcccctctc tacttcctcc ctccagtccc 60

ttctccatcc ctcccttttt tggctgcccc ttgcctgcct tcctcgccag tagcttgcag 120

agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180

agccaccatg gaggaccaag                                               200


<210> 20
<211> 69
<212> DNA
<213> Homo sapiens

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